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RAW SEQUENCE LISTING DATE: 12/01/2000
PATENT APPLICATION: US/09/714,865 TIME: 13:28:55

Input Set : A:\B8017195.txt
Output Set: N:\CRF3\12012000\I714865.raw

4 <110> APPLICANT: Castrillon, Diego H.
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
6 IMPROVED DIAGNOSIS OF GERM CELL TUMORS
7
11 <130> FILE REFERENCE: B0801/7195/ERP/KA
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/714,865
C--> 13 <141> CURRENT FILING DATE: 2000-11-16
13 <150> PRIOR APPLICATION NUMBER: U.S. 60/166,394
14 <151> PRIOR FILING DATE: 1999-11-18
16 <160> NUMBER OF SEQ ID NOS: 15
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2224
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo Sapiens
25 <400> SEQUENCE: 1
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27 ctatgttccc atatttgaga aqgataggtt ttctggagaa aatggagaca at
28 gactccagct tcatacatcg aaatggatga tggacettct cgaagagatc at
29 aagtqatttgc gctctgggc ggaattttgg aaacagagatc gctgttgatc gt
30 agataataaca tccacaatgg gtgtttttgg aqgttggaaag aqgttttggaa ac
31 ttc当地acgc aqgttggaaat gatgttqatag ctctgttttc tgagagatg ct
32 ctgc当地aaat aatccaaacac ggaacagagg gtttccaaag aqaggccgatc at
33 aaataattca gaagcttccag ggc当地atcag aagagggttga agaggtagtt tc
34 ccgtqaggaa tt当地gttctag gaagttccaaat taatgactta gacccagaaq aa
35 ggc当地acttgg ggc当地tttgc gttctttagaag accagttata aqgttggccatc gt
36 tacttcttca aqgcaagatg gcaatggaaat gtttccaaat ggttacaaatg g
37 agaagtaata acaggcttcg aqgaaatccat tt当地ggatca gaagcagaaat g
38 tagtqataact caaggacaa aqgtqaccta catacccccct cttccacatcg ag
39 ctccatctttt gcaatatttcc agacaggcat aqaaatccgac aatatacgacatc ct
40 ggaatgttctt ggc当地atgttgc caccatccggc aatttctgact tt当地ggaaatg ct
41 tc当地agactt aataacaacaat tt当地ttaaagc tggatataact aqgttacttc ct
42 atacatgttatttccatcatc tt当地ggggccatc agatgttgc tggatgttgc t
43 tt当地ggaaatg gccc当地tttc tt当地ttaaagatc tt当地ggatcat atgatgcatg at
44 tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc ca
45 attgggcaac cagatatttttggatccatccggc aatattttctt tt当地ggggccatc gt
46 tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt
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50 aaccctttagt tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt
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52 gcaatggatccatc tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt
53 aaacatgggg gatggaaatggaa tt当地ggggccatc tt当地ggggccatc tt
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55 gagagagccg gggatggatccatc tt当地ggggccatc tt当地ggggccatc tt
56 tacttcttca tt当地ggggccatc tt当地ggggccatc tt当地ggggccatc tt
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58 tactggcaga gcaatttctt tttttgatct tgaatcggat aaccattttag cacagcctct 1980
 59 agttaaaatgtt ttgacatgtt ctcaacaggtt tggttggaaat aaattgcit 2040
 60 tagtacatac attccctggct tcagtggtag tacaayagga aacgtgttgc catcagtta 2100
 61 taccagaaatggcaagagca ctttgaacac agctgggtttt tctttttcac gagctccaa 2160
 62 tccagtagat gatgagtcat gggattaaag cccaaacatc cttcaagtctt gtggtttga 2220
 63 tgca 2224
 65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 724
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Homo Sapiens
 70 <400> SEQUENCE: 2
 71 Met Gly Asp Glu Asp Trp Glu Ala Glu Ile Asn Pro His Met Ser Ser
 72 1 5 10 15
 73 Tyr Val Pro Ile Phe Glu Lys Asp Arg Tyr Ser Gly Glu Asn Gly Asp
 74 20 25 30
 75 Asn Phe Asn Arg Thr Pro Ala Ser Ser Ser Glu Met Asp Asp Gly Pro
 76 35 40 45
 77 Ser Arg Arg Asp His Phe Met Lys Ser Gly Phe Ala Ser Gly Arg Asn
 78 50 55 60
 79 Phe Gly Asn Arg Asp Ala Gly Glu Cys Asn Lys Arg Asp Asn Thr Ser
 80 65 70 75 80
 81 Thr Met Gly Gly Phe Gly Val Gly Lys Ser Phe Gly Asn Arg Gly Phe
 82 85 90 95
 83 Ser Asn Ser Arg Phe Glu Asp Gly Asp Ser Ser Gly Phe Trp Arg Glu
 84 100 105 110
 85 Ser Ser Asn Asp Cys Glu Asp Asn Pro Thr Arg Asn Arg Gly Phe Ser
 86 115 120 125
 87 Lys Arg Gly Gly Tyr Arg Asp Gly Asn Asn Ser Glu Ala Ser Gly Pro
 88 130 135 140
 89 Tyr Arg Arg Gly Gly Arg Gly Ser Phe Arg Gly Cys Arg Gly Gly Phe
 90 145 150 155 160
 91 Gly Leu Gly Ser Pro Asn Asn Asp Leu Asp Pro Asp Glu Cys Met Gln
 92 165 170 175
 93 Arg Thr Gly Gly Leu Phe Gly Ser Arg Arg Pro Val Leu Ser Gly Thr
 94 180 185 190
 95 Gly Asn Gly Asp Thr Ser Gln Ser Arg Ser Gly Ser Gly Ser Glu Arg
 96 195 200 205
 97 Gly Gly Tyr Lys Gly Leu Asn Glu Glu Val Ile Thr Gly Ser Gly Lys
 98 210 215 220
 99 Asn Ser Trp Lys Ser Glu Ala Glu Gly Gly Glu Ser Ser Asp Thr Gln
 100 225 230 235 240
 101 Gly Pro Lys Val Thr Tyr Ile Pro Pro Pro Pro Glu Asp Glu Asp
 102 245 250 255
 103 Ser Ile Phe Ala His Tyr Gln Thr Gly Ile Asn Phe Asp Lys Tyr Asp
 104 260 265 270
 105 Thr Ile Leu Val Glu Val Ser Gly His Asp Ala Pro Pro Ala Ile Leu
 106 275 280 285
 107 Thr Phe Glu Glu Ala Asn Leu Cys Gln Thr Leu Asn Asn Asn Ile Ala
 108 290 295 300

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109 Lys Ala Gly Tyr Thr Lys Leu Thr Pro Val Gln Lys Tyr Ser Ile Pro
110 305 310 315 320
111 Ile Ile Leu Ala Gly Arg Asp Leu Met Ala Cys Ala Gln Thr Gly Ser
112 325 330 335
113 Gly Lys Thr Ala Ala Phe Leu Leu Pro Ile Leu Ala His Met Met His
114 340 345 350
115 Asp Gly Ile Thr Ala Ser Arg Phe Lys Glu Leu Gln Glu Pro Glu Cys
116 355 360 365
117 Ile Ile Val Ala Pro Thr Arg Glu Leu Val Asn Gln Ile Tyr Leu Glu
118 370 375 380
119 Ala Arg Lys Phe Ser Phe Gly Thr Cys Val Arg Ala Val Val Ile Tyr
120 385 390 395 400
121 Gly Gly Thr Gln Leu Gly His Ser Ile Arg Gln Ile Val Gln Gly Cys
122 405 410 415
123 Asn Ile Leu Cys Ala Thr Pro Gly Arg Leu Met Asp Ile Ile Gly Lys
124 420 425 430
125 Glu Lys Ile Gly Leu Lys Gln Ile Lys Tyr Leu Val Leu Asp Glu Ala
126 435 440 445
127 Asp Arg Met Leu Asp Met Gly Phe Gly Pro Glu Met Lys Lys Leu Ile
128 450 455 460
129 Ser Cys Pro Gly Met Pro Ser Lys Glu Gln Arg Gln Thr Leu Met Phe
130 465 470 475 480
131 Ser Ala Thr Phe Pro Glu Glu Ile Gln Arg Leu Ala Ala Glu Phe Leu
132 485 490 495
133 Lys Ser Asn Tyr Leu Phe Val Ala Val Gly Gln Val Gly Gly Ala Cys
134 500 505 510
135 Arg Asp Val Gln Gln Thr Val Leu Gln Val Gly Gln Phe Ser Lys Arg
136 515 520 525
137 Glu Lys Leu Val Glu Ile Leu Arg Asn Ile Gly Asp Glu Arg Thr Met
138 530 535 540
139 Val Phe Val Glu Thr Lys Lys Ala Asp Phe Thr Ala Thr Phe Leu
140 545 550 555 560
141 Cys Gln Glu Lys Ile Ser Thr Thr Ser Ile His Gly Asp Arg Glu Gln
142 565 570 575
143 Arg Glu Arg Glu Gln Ala Leu Gly Asp Phe Arg Phe Gly Lys Cys Pro
144 580 585 590
145 Val Leu Val Ala Thr Ser Val Ala Ala Arg Gly Leu Asp Ile Glu Asn
146 595 600 605
147 Val Gln His Val Ile Asn Phe Asp Leu Pro Ser Thr Ile Asp Glu Tyr
148 610 615 620
149 Val His Arg Ile Gly Arg Thr Gly Arg Cys Gly Asn Thr Gly Arg Ala
150 625 630 635 640
151 Ile Ser Phe Phe Asp Leu Glu Ser Asp Asn His Leu Ala Gln Pro Leu
152 645 650 655
153 Val Lys Val Leu Thr Asp Ala Gln Gln Asp Val Pro Ala Trp Leu Glu
154 660 665 670
155 Glu Ile Ala Phe Ser Thr Tyr Ile Pro Gly Phe Ser Gly Ser Thr Arg
156 675 680 685
157 Gly Asn Val Phe Ala Ser Val Asp Thr Arg Lys Gly Lys Ser Thr Leu

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158 690 695 700
 159 Asn Thr Ala Gly Phe Ser Ser Ser Arg Ala Pro Asn Pro Val Asp Asp
 160 705 710 715 720
 161 Glu Ser Trp Asp
 164 <210> SEQ ID NO: 3
 165 <211> LENGTH: 722
 166 <212> TYPE: PRT
 167 <213> ORGANISM: Mus Musculus
 169 <400> SEQUENCE: 3
 170 Met Gly Asp Glu Asp Trp Glu Ala Glu Ile Leu Lys Pro His Val Ser
 171 1 5 10 15
 172 Ser Tyr Val Pro Val Phe Glu Lys Asp Lys Tyr Ser Ser Gly Ala Asn
 173 20 25 30
 174 Gly Asp Thr Phe Asn Arg Thr Ser Ala Ser Ser Glu Met Glu Asp Gly
 175 35 40 45
 176 Pro Ser Gly Arg Asp Asp Phe Met Arg Ser Gly Phe Pro Ser Gly Arg
 177 50 55 60
 178 Ser Leu Gly Ser Arg Asp Ile Gly Glu Ser Ser Lys Lys Glu Asn Thr
 179 65 70 75 80
 180 Ser Thr Thr Gly Gly Phe Gly Arg Gly Lys Gly Phe Gly Asn Arg Gly
 181 85 90 95
 182 Phe Leu Asn Asn Lys Phe Glu Glu Asp Ser Ser Gly Phe Trp Lys
 183 100 105 110
 184 Glu Ser Asn Asn Asp Cys Glu Asp Asn Gln Thr Arg Ser Arg Gly Phe
 185 115 120 125
 186 Ser Lys Arg Gly Gly Cys Gln Asp Gly Asn Asp Ser Glu Ala Ser Gly
 187 130 135 140
 188 Pro Phe Arg Arg Gly Gly Arg Gly Ser Phe Arg Gly Cys Arg Gly Gly
 189 145 150 155 160
 190 Phe Gly Leu Gly Arg Pro Asn Ser Glu Ser Asp Gln Asp Gln Gly Thr
 191 165 170 175
 192 Gln Cys Gly Gly Phe Leu Val Leu Gly Lys Pro Ala Ala Ser Asp
 193 180 185 190
 194 Ser Gly Asn Gly Asp Thr Tyr Gln Ser Arg Ser Gly Ser Gly Arg Gly
 195 195 200 205
 196 Gly Tyr Lys Gly Leu Asn Glu Glu Val Val Thr Gly Ser Gly Lys Asn
 197 210 215 220
 198 Ser Trp Lys Ser Glu Thr Glu Gly Gly Glu Ser Ser Asp Ser Gln Gly
 199 225 230 235 240
 200 Pro Lys Val Thr Tyr Ile Pro Pro Pro Pro Glu Asp Glu Asp Ser
 201 245 250 255
 202 Ile Phe Ala His Tyr Gln Thr Gly Ile Asn Phe Asp Lys Tyr Asp Thr
 203 260 265 270
 204 Ile Leu Val Glu Val Val Ser Gly His Asp Ala Pro Pro Ala Ile Leu Thr
 205 275 280 285
 206 Phe Glu Glu Ala Asn Leu Cys Gln Thr Leu Asn Asn Asn Ile Arg Lys
 207 290 295 300
 208 Ala Gly Tyr Thr Lys Leu Thr Pro Val Gln Lys Tyr Thr Ile Pro Ile
 209 305 310 315 320

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210 Val Leu Ala Gly Arg Asp Leu Met Ala Cys Ala Gln Thr Gly Ser Gly
 325 330 335
 211 Lys Thr Ala Ala Phe Leu Leu Pro Ile Leu Ala His Met Met Arg Asp
 340 345 350
 212 Gly Ile Thr Ala Ser Arg Phe Lys Glu Leu Gln Glu Pro Glu Cys Ile
 355 360 365
 213 Ile Val Ala Pro Thr Arg Glu Leu Ile Asn Gln Ile Tyr Leu Glu Ala
 370 375 380
 214 Arg Lys Phe Ser Phe Gly Thr Cys Val Ile Ser Val Val Ile Tyr Gly
 385 390 395 400
 215 Gly Thr Gln Phe Gly His Ser Val Arg Gln Ile Val Gln Gly Cys Asn
 405 410 415
 216 Ile Leu Cys Ala Thr Pro Gly Arg Leu Met Asp Ile Ile Gly Lys Glu
 420 425 430
 217 Lys Ile Gly Leu Lys Gln Val Lys Tyr Leu Val Leu Asp Glu Ala Asp
 435 440 445
 218 Ser Met Leu Asp Met Gly Phe Ala Pro Glu Ile Lys Lys Leu Ile Ser
 450 455 460
 219 Cys Pro Gly Met Pro Ser Lys Glu Gln His Gln Thr Leu Leu Phe Ser
 465 470 475 480
 220 Ala Thr Phe Pro Glu Glu Ile Gln Arg Leu Ala Gly Asp Phe Leu Lys
 485 490 495
 221 Ser Asn Tyr Leu Phe Val Ala Val Gly Gln Val Gly Gly Ala Cys Arg
 500 505 510
 222 Asp Val Gln Gln Thr Ile Leu Gln Val Gly Gln Tyr Gln Lys Glu Lys
 515 520 525
 223 Ser Leu Leu Arg Phe Tyr Glu Asn Ile Gly Asp Glu Arg Thr Met Val
 530 535 540
 224 Phe Val Glu Thr Lys Lys Ala Asp Phe Ile Ala Thr Phe Leu Cys
 545 550 555 560
 225 Gln Glu Lys Ile Ser Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg
 565 570 575
 226 Glu Arg Glu Gln Ala Leu Gly Asp Phe Arg Cys Gly Lys Cys Pro Val
 580 585 590
 227 Leu Val Ala Thr Ser Val Ala Ala Arg Gly Leu Asp Ile Glu Asn Val
 595 600 605
 228 Gln His Val Ile Asn Phe Asp Leu Pro Ser Thr Ile Asp Glu Tyr Val
 610 615 620
 229 His Arg Ile Gly Arg Thr Gly Arg Cys Gly Asn Thr Gly Arg Ala Ile
 625 630 635 640
 230 Ser Phe Phe Asp Thr Asp Ser Asp Asn His Leu Ala Gln Pro Leu Val
 645 650 655
 231 Lys Val Leu Ser Asp Ala Gln Gln Asp Val Pro Ala Trp Leu Glu Glu
 660 665 670
 232 Ile Ala Phe Ser Thr Tyr Val Pro Pro Ser Phe Ser Ser Ser Thr Arg
 675 680 685
 233 Gly Gly Ala Val Phe Ala Ser Val Asp Thr Arg Lys Asn Tyr Gln Gly
 690 695 700
 234 Lys Ala His Val Glu Tyr Ser Gly Asp Phe Phe Thr Ser Ser Gln

VERIFICATION SUMMARY
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date